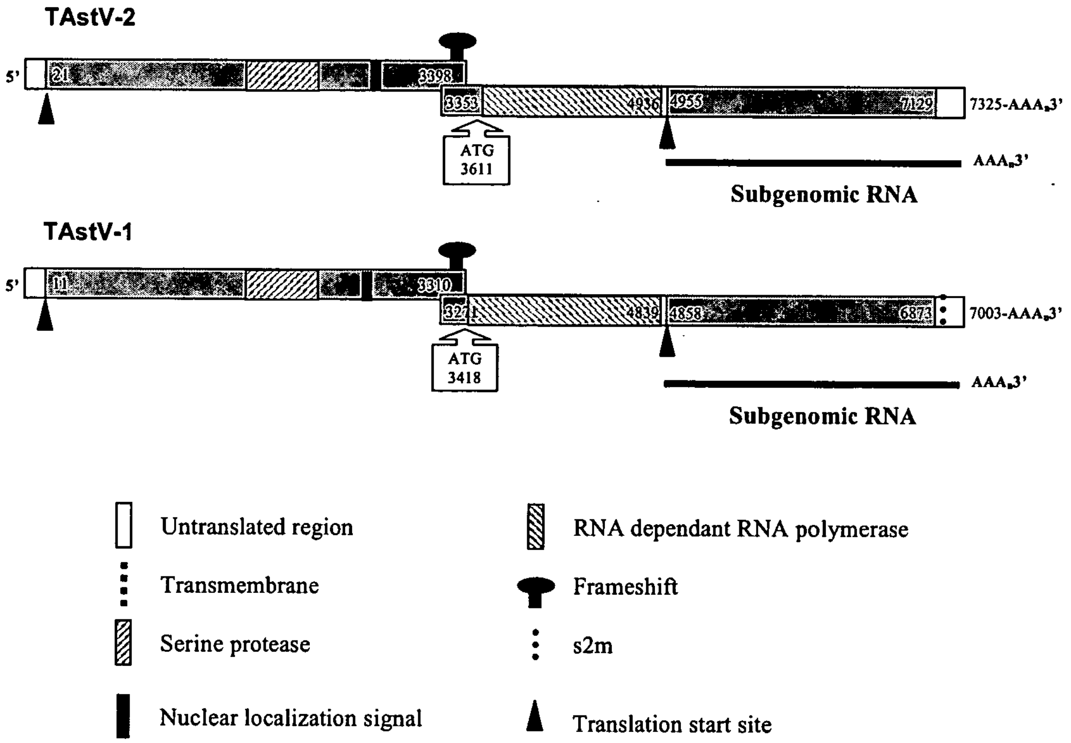
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AAAn3'
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Untranslated region
RNA dependant RNA polymerase
Transmembrane
Frameshift
Serine protease
s2m
Nuclear localization signal
Translation start site

Fig 1

Fig 2A

SEQ ID NO:7

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Fig 2B

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Fig 2C

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               701                                                750
 TAstV2_2.seq  CCTGGTGACA GCCCAACTGA TTCTCTTGGG CCAGCACTCA ACATGTGGAC
  CA_ORF2.seq  CCTGGTGACA GCCCAACTGA TTCTCTTGGG CCAGCACTCA ACATGTGGAC
  PA_ORF2.seq  CCTGGTGACA GCCCAACTGA TTCTCTTGGG CCAGCACTCA ACATGTGGAC
  MI_ORF2.seq  CCCGGTGACA GCCCAACTGA TTCTCTTGGG CCAGCACTCA ATATGTGGAC
  TX_ORF2.seq  CCTGGTGACA GCCCAACTGA TTCCCTTGGG CCAGCACTCA ACATGTGGAC
  MN_ORF2.seq  CCTGGTGATA GTCCAACTGA TTCTCTTGGA CCGGCACTTA ACATGTGGAC
    Consensus  CCtGGTGAcA GcCCAACTGA TTCtCTTGGg CCaGCACTcA AcATGTGGAC

               751                                                800
 TAstV2_2.seq  CTACCTGCAA ACTGTCAATG CACTCCAGAG CGCTGGGGGC ACTCAAACGC
  CA_ORF2.seq  CTACCTGCAA ACTGTCAATG CACTCCAGAG CGCTGGGGGC AACCAAACGC
  PA_ORF2.seq  CTACCTGCAA ACTGTCAATG CACTCCAGAG CGCCACTGGT ACACAAACAC
  MI_ORF2.seq  CTACCTGCAA ACTGTCAATG CACTCCAGAG CACCAGTGGT ACACAAACAC
  TX_ORF2.seq  CTACCTGCAA ACTGTTAATG CACTCCAGAG CGCTGGGGGC AACCAAACAC
  MN_ORF2.seq  TTATTTGCAA ACTGTCAATG CACTCCACAG CAATAACGGC ACACAAACAC
    Consensus  cTAccTGCAA ACTGTcAATG CACTCCAgAG Cgctag.GGc AcaCAAACaC

               801                                                850
 TAstV2_2.seq  CTTACACCAG TGCACTTTTT CTTGTGGAGG TCTTGGTCAC TTATGAGTTT
  CA_ORF2.seq  CTTACACCAG TGCACTTTTC CTTGTGGAGG TCTTGGTTAC TTATGAGTTT
  PA_ORF2.seq  CGTACACCAG TGCACTTTTC CTTGTGGAGG TCTTGGTTAC GTATGAGTTT
  MI_ORF2.seq  CTTATACCAG TGCACTTTTC CTTGTGGAGG TTTTGGTTAC TTATGAGTTT
  TX_ORF2.seq  CTTACACCAG TGCACTTTTC CTTGTGGAGG TCTTGGTTAC CTATGAGTTT
  MN_ORF2.seq  CTTACACCAG TGCACTTTTC CTTGTGGAGG TCTTGGTCAC ATATGAGTTT
    Consensus  CtTAcACCAG TGCACTTTTc CTTGTGGAGG TcTTGGTtAC .TATGAGTTT
```

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              851                                                 900
TAstV2_2.seq  TCAAACTATG GCCCAAAGCC TGCACTGTCT CAAATGGTAT CAGACAGCTT
 CA_ORF2.seq  TCAAACTATG GTCCAAAGCC TGCACTGTCT CAAATGGTAT CAGATAGTTT
 PA_ORF2.seq  TCAAATTATG GTCCAAAGCC CGCACTGTCC CAGATGGTAT CAGACAGCTT
 MI_ORF2.seq  TCAAATTATG GTCCAAAGCC CGCACTGTCC CAGATGGTAT CAGACAGCTT
 TX_ORF2.seq  TCAAATTATG GTCCAAAGCC TGCACTGTCC CAAATGATAT CGGACAGTTT
 MN_ORF2.seq  TCAAACTATG GTCCCAAACC TGCACTGTCC CAGATGATTT CGGATAGCTT
   Consensus  TCAAAcTATG GtCCaAAgCC tGCACTGTCc CAgATGgTaT CaGAcAGcTT

              901                                                 950
TAstV2_2.seq  TCCACCAGCC TCCGGTTCTA CTGCAACCTT AAAAAACACC AGTGATGGGG
 CA_ORF2.seq  TCCACCATCC TCCGGTTCTA CTGCAACCCT AAAAAACACC AGTGATGGGG
 PA_ORF2.seq  TCCACCAGCT TCCGGCTCTA CTGCAACCTT AAAAAACACC AGTGATGGGG
 MI_ORF2.seq  TCCACCAGCT TCCGGCTCTA CTGCAACCTT AAAAAACACC AGTGATGGGG
 TX_ORF2.seq  TCCACCAGCC TCCGGTTCTA CTGCAACTCT TAAAAACACC AGTGATGGGG
 MN_ORF2.seq  TCCACCAGCT GCTGGTTCAA CTGCAACTCT AAAAAACACC AGTGATGGGG
   Consensus  TCCACCAgCt tCcGGtTCtA CTGCAACccT aAAAAACACC AGTGATGGGG

              951                                                1000
TAstV2_2.seq  CTGTAGCAAT ACAACTCTCA GGCGCTATCG CCCGAAAGAT GGAGGAGGTT
 CA_ORF2.seq  CTGTAGCAAT ACAACTCTCA GGCGCTATCG CCCGAAAGAT GGAGGAGGTT
 PA_ORF2.seq  CTGTAGCAAT ACAACTCTCA GGCGCTATTG CCCGAAAGAT GGAGGAGGTT
 MI_ORF2.seq  CTGTAGCAAT ACAACTCTCA GGCGCTATTG CCCGAAAGAT GGAGGAGGTT
 TX_ORF2.seq  CTGTAGCAAT ACAACTTTCA GGCGCTATCG CCCGAAAAAT GGAGGAGCTT
 MN_ORF2.seq  CTGTTGCAGT GCAGCTTTCG GGTGCTATCG CCCGTAGGAT GGAGGAGGTT
   Consensus  CTGTaGCAaT aCAaCTcTCa GGcGCTATcG CCCGaAagAT GGAGGAGgTT

              1001                                               1050
TAstV2_2.seq  GAGCCCAAGG GTAGGCGCTC AAATGCGCAA ACATCAGGTG TCGGTGAAGT
 CA_ORF2.seq  GAGCCCAAGG TTAGGCGCTC AAATGCGCAA ACATCAGGTG TCGGTGAAGT
 PA_ORF2.seq  GAGCCCAAGG GTAGGCGCTC AAATGCGCAA ACATCAGGTG TCGGTGAAGT
 MI_ORF2.seq  GAGCCCAAGG GTAGGCGCTC AAATGCGCAA ACATCAGGTG TCGGTGAAGT
 TX_ORF2.seq  GAGCCTAAGG GTAGATGCTC AAATGCACAG ACATCAGGTG TTGGAGAAGT
 MN_ORF2.seq  GAACCTAAGA GCAGGCGGTC AAATGCACAG ACATCAGGTG TTGGAGAAGT
   Consensus  GAgCCcAAGg gtAGgcGcTC AAATGCgCAa ACATCAGGTG TcGGtGAAGT

              1051                                               1100
TAstV2_2.seq  GTTCTGGGCA GTGTCCACTG AAGTAGTCAA TACAGTAGCA GATGCCATAC
 CA_ORF2.seq  GTTCTGGGCA GTGTCCACTG AAGTAGTCAA TACAGTAGCA GATGCCATAC
 PA_ORF2.seq  GTTCTGGGCA GTGTCCACTG AAGTGGTCAA CACAGTAGCA GATGCCATAC
 MI_ORF2.seq  GTTCTGGGCA GTGTCCACTG AAGTAGTCAA TACAGTAGCA GATGCCATAC
 TX_ORF2.seq  GTTTTGGGCA GTGTCAACTG AGGTGGTTAA CACAGTAGCA GATGCTATAC
 MN_ORF2.seq  GTTTTGGGCA GTGTCAACTG ATGTAGTTAA CACAGTAGCA GATGCTATAC
   Consensus  GTTcTGGGCA GTGTCcACTG AaGTaGTcAA cACAGTAGCA GATGCcATAC

              1101                                               1150
TAstV2_2.seq  CAGGCTGGGG CTGGCTCCTG AAAGGTGGCT GGTTTGTCCT TAGGAAAATC
 CA_ORF2.seq  CAGGCTGGGG CTGGCTCCTG AAGGGTGGCT GGTTTGTCCT CAGGAAAATC
 PA_ORF2.seq  CAGGCTGGGG CTGGCTCCTG AAAGGTGGCT GGTTTGTCCT CAGGAAAATC
 MI_ORF2.seq  CAGGCTGGGG CTGGCTCCTG AAAGGTGGCT GGTTTGTCCT CAGGAAAATT
 TX_ORF2.seq  CAGGTTGGGG TTGGCTCTTG AAAGGTGGCT GGTTTGTCCT TAGAAAATTA
 MN_ORF2.seq  CAGGCTGGGG TTGGCTCCTG AAAGGTGGCT GGTTCGTCCT TAGGAAGATA
   Consensus  CAGGcTGGGG cTGGCTCcTG AAaGGTGGCT GGTTtGTCCT tAGgAAaaT.
```

```
              1151                                               1200
TAstV2_2.seq  TTTGGGGCCG CAAATGACCA GAATGGCACT TACTTGATAT ACTCTTCAGT
 CA_ORF2.seq  TTTGGGGCCG CGAATGACCA GAATGGCACT TACTTGATAT ACTCTTCAGT
 PA_ORF2.seq  TTTGGGGCCG CGAATGACCA GAATGGCACT TACTTGATAT ACTCTTCAGT
 MI_ORF2.seq  TTTGGGGCCG CGAATGACCA GAATGGCACT TACTTGATAT ACTCTTCAGT
 TX_ORF2.seq  TTTGGAGCTG CGAATGACGC AAATGGCACC TACCTGTTAT ATTCATCGGT
 MN_ORF2.seq  TTTGGAGCTG CGAATGACGC AAATAGCACC TACCTGTTGT ATTCATCGGT
   Consensus  TTTGGgGCcG CgAATGACca gAATgGCACt TACtTGaTaT AcTCtTCaGT

              1201                                               1250
TAstV2_2.seq  GGCAGATGCA CAAGGTGACA ACAGGATATA CACATCAGTG AAACAGACAC
 CA_ORF2.seq  GGCAGATGCA CAAGGTGACA ACAGGATATA CACATCAGTG AAACAGACAC
 PA_ORF2.seq  GGCAGATGCA CAAGGTGACA ACAGGATATA CACATCAGTG AAACAGACAC
 MI_ORF2.seq  GGCAGATGCA CAAGGTGACA ACAGGATATA CACTTCAGTG AAACAGACAC
 TX_ORF2.seq  GGCCGATGCA CAGCAGGATA ACAGATTATA TACAAAAGTG AAACAAGGAC
 MN_ORF2.seq  AGCTGATGCA CAGCAAGACA ACAGAATATA TACAACAATA AAACAAGGAC
   Consensus  gGCaGATGCA CAaggtGAcA ACAGgaTATA cACatcAgTg AAACAgacAC

              1251                                               1300
TAstV2_2.seq  AG......TT GACATCAAGC AGGATCAACC TCGTCCAACT CACCCAGCCC
 CA_ORF2.seq  AG......TT GACATCAAGC AGGATCAACC TCGTCCAACT CACCCAGCCC
 PA_ORF2.seq  AG......TT GACATCAAGC AGGATCAACC TCGTCCAACT CACCCAGCCC
 MI_ORF2.seq  AG......TT GATATCAAGC AGGATCAACC TCGTCCAGCT CACCCAGCCC
 TX_ORF2.seq  AA......TT AACATCGAGT GTGATCAACC TCGTCCAACT CACTCAGCCC
 MN_ORF2.seq  AAGGACAACT AACATCAAGT GTGATCAATC TGGTTCAACT CACCCAGCCA
   Consensus  Ag......tT gAcATCaAGc agGATCAAcC TcGTcCAaCT CACcCAGCCc

              1301                                               1350
TAstV2_2.seq  AATGTGAACC AAGCAGCAGT AGGTGGCAGT GTTGGTGCGG CAAACTCCAT
 CA_ORF2.seq  AATGTGAACC AAGCAGCAGT AGGTGGCAGT GTTGGTGCGG CAAACTCTAT
 PA_ORF2.seq  AATGTGAACC AAGCAGCAGT AGGTGGCAGT GTTGGTGCGG CAAACTCCAT
 MI_ORF2.seq  AATGTGAACC AAGCAGCAGT AGGTGGCAGT GTTGGCACGG CAAACTCCAT
 TX_ORF2.seq  AATGTGAACC AAGCAGCAGT AGGTGGCAGT GTTGGCTCGG CAAATTCCAT
 MN_ORF2.seq  AATGTAAATC AAGCAGCTGT TGGTGGTAGT GTTGGTTCTG CAAATTCCAT
   Consensus  AATGTgAAcC AAGCAGCaGT aGGTGGcAGT GTTGGt.CgG CAAAcTCcAT

              1351                                               1400
TAstV2_2.seq  CTATTTGCCA CTACCACAAG CAGATGACCA ATACACACCC TACTTTGTCT
 CA_ORF2.seq  ATATTTGCCA CTACCACAAG CAGATGACCA ATATACACCC TACTTTGTCT
 PA_ORF2.seq  CTATTTGCCA CTGCCACAAG CAGATGATCA ATACACACCC TATTTTGTTT
 MI_ORF2.seq  CTACTTGCCA CTACCACAAG CAGATGATCA ATACACACCC TATTTTGTTT
 TX_ORF2.seq  CTATTTGCCA TTACCACAAG CAGATGACCA ATATACACCC CATCTTGTTT
 MN_ORF2.seq  CTACCTACCC TTGCCACAAG CAGAGGATCA ATATACACCG CACTTTGTTT
   Consensus  cTAttTgCCa cTaCCACAAG CAGAtGAtCA ATAtACACCc tActTTGTtT

              1401                                               1450
TAstV2_2.seq  ATAATTTTCA AGGGGAAAGG GTGTCAACCA CCGAGACTGG GGTATTTTGT
 CA_ORF2.seq  ATAATTTTCA AGGGGAAAGG GTGTCAACCA CCGAGACTGG GGTATTTTGT
 PA_ORF2.seq  ATAATTTTCA AGGGGAAAGG GTGTCAACCA CCGAGACTGG GGTATTTTGT
 MI_ORF2.seq  ATAATTTTCA AGGGGATAGG GTGTCAACCA CCGAAACTGG GGTATTTTGT
 TX_ORF2.seq  ATGATTTCCA AGGGAATAGG GTGTCAACCG CTGAGACTGG GGTATTTTGT
 MN_ORF2.seq  ATGATTTCCA GGGAACGAGG GTGTCAACAA CAGAGTCTGG AGTCTTTTGC
   Consensus  ATaATTTtCA aGGgga.AGG GTGTCAACca CcGAgaCTGG gGTaTTTTGt
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               1451                                              1500
TAstV2_2.seq   CTGGCAGCCA TACCAGCTGC GACTACATCT AGTAGGTATA ATAATCAGAT
  CA_ORF2.seq  TTGGCAGCCA TACCAGCTGC GACTACATCC AGTAGGTATA ATAATCAGAT
  PA_ORF2.seq  CTGGCAGCCA TACCAGCAGC GACTACAACT AGTAGGTATA ATAATCAGAT
  MI_ORF2.seq  CTGGCAGCCA TACCAGCTGC GACTACAACT AGTAGGTATA ATAATCAGAT
  TX_ORF2.seq  CTGGCATCCA TACCAGCCGC AACTACATCC AGTAGGTACA ATGGTCAAAT
  MN_ORF2.seq  CTGTCCTCAA TACCAAGTGC TGACAGTAAG AGCAGATATA ACAACCAGAT
    Consensus  cTGgCagCcA TACCAgctGC gactAcaac. AGtAGgTAtA AtaatCAgAT

               1501                                              1550
TAstV2_2.seq   CACCACTCCA TCAATTGGCT ACAGGAATGC TAGTGGTACA GGAACATCAT
  CA_ORF2.seq  CACCACTCCA TCAATAGGCT ACAGGAATGC TAGTGGTACA GGAACATCAT
  PA_ORF2.seq  CACCACTCCA TCAATTGGCT ACAGGAATGA TAGTGGTACA GGAACATCAT
  MI_ORF2.seq  TACCACTCCA TCAATTGGCT ACAGGAATGC TAGTGGTACA GGAACATCAT
  TX_ORF2.seq  CACCAGTCCT TCAATTGGCT ATAAGAGTGC TAGTGGCACA GGAACATCTT
  MN_ORF2.seq  GAACTCTCCA ACAGTGGGAT ATAAGAATGA AGGTGGTACT GGAACATCAT
    Consensus  cAcCacTCCa tCAaTtGGcT AcAgGAaTGc taGTGGtACa GGAACATCaT

               1551                                              1600
TAstV2_2.seq   TCCTACTAGA TGCTGCATCA TGGTGGAATA TATTGGATGT AACTCAGACT
  CA_ORF2.seq  TCCTACTAGA TGCTGCATCA TGGTGGAATA TATTGGATGT AACTCAGACT
  PA_ORF2.seq  TCCTACTAGA TGCTGCATCA TGGTGGAATA TATTGGATGT AACTCAAACT
  MI_ORF2.seq  TCCTACTAGA TGCTGCATCA TGGTGGAATA TATTGGATGT AACTCAGACT
  TX_ORF2.seq  TCTCACTAGA TGAAGCATCA TGGTGGAACA TCTTGGATGT AACTCAGACT
  MN_ORF2.seq  TCGCTATGGA CAATGCCCCG TGGTGGAGCA TCCTGGATGT TACTCAAACA
    Consensus  TCctacTaGA tgctGCatCa TGGTGGAatA TatTGGATGT aACTCAgACt

               1601                                              1650
TAstV2_2.seq   GGAGTGCTTT TTGGACAACC AAGATTGGGT GTTGGTGTCA TGCAGACAAT
  CA_ORF2.seq  GGAGTGCTCT TTGGACAACC AAGATTGGGT GTTGGTGTTA TGCAGACAAT
  PA_ORF2.seq  GGAGTGCTCT TTGGACAACC AAGATTGGGT GTTGGTGTCA TGCAGACAAT
  MI_ORF2.seq  GGAGTGCTCT TTGGACAACC AAGATTGGGT GTTGGTGTTA TGCAGACAAT
  TX_ORF2.seq  GGGGTCCTCT TTGGACAACC AAAATTGGGC ATTGGTGTCA TGCAAACAAT
  MN_ORF2.seq  GGTGTCATCT TTGGCCAGCC CAGGTTAGGT GTTGGGGTTA TACAAACAAT
    Consensus  GGaGTgcTcT TTGGaCAaCC aAgaTTgGGt gTTGGtGTtA TgCAgACAAT

               1651                                              1700
TAstV2_2.seq   GAAGACTCTC AAACAGCATA TCAAGGATTA CACAGAGCCT GCAATACAGA
  CA_ORF2.seq  GAAGACTCTC AAACAGCATA TCAAGGATTA CACAGAGCCT GCAATACAGA
  PA_ORF2.seq  GAAGACTCTT AAACAGCATA TCAAGGATTA TACAGAGCCT GCAATACAGA
  MI_ORF2.seq  GAAGACTCTT AAACAGCATA TCAAGGATTA CACAGAGCCT GCAATACAGA
  TX_ORF2.seq  GAAGACCCTT AAACAACACA TCAGGGATTA TACAGAGCCT GCAATAAAAA
  MN_ORF2.seq  GAAAACACTG AAACAACACA TTACAGATTT TACTGAACCT GCAGTAAAGA
    Consensus  GAAgACtCT. AAACAgCAtA TcAagGATTa tACaGAgCCT GCAaTAcAgA

               1701                                              1750
TAstV2_2.seq   AATATTATCC TGGAACAACT AACCTTGATG AGCAGTTGAA GCAGAGATTG
  CA_ORF2.seq  AATATTATCC TGGAACAACC AACCTTGATG AGCAGTTGAA ACAGAGAYTG
  PA_ORF2.seq  AATATTATCC TGGAACAACC AACCTTGATG AGCAGTTGAA ACAGAGATTG
  MI_ORF2.seq  AATATTATCC TGGAACAACC AACCTTGATG AGCAGTTGAA ACAGAGATTG
  TX_ORF2.seq  AATATTACCC TGGAACAACT AACATTGCTG AAGAATTGAA ACAGAGGATG
  MN_ORF2.seq  AATATTATCC TGGCACTACC AACTTGGACC AGACACTCAA AGATAGAATG
    Consensus  AATATTAtCC TGGaACaACc AACcTtGatg AgcagtTgAA acAgAGa.TG
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                1751                                               1800
  TAstV2_2.seq  AACCTGGCAG AGGGTGACCC GGTCATCTCA ATGGGGGACA CAAACGGTAG
   CA_ORF2.seq  AACCTGGCAG AGGGTGACCC GGTCATCTCA ATGGGGGACA CAACCGGTAG
   PA_ORF2.seq  AACCTGGCAG AGGGTGACCC GGTCATCTCA ATGGGGGACA CAACCGGTAG
   MI_ORF2.seq  AACCTGGCAG AGGGTGACCC GGTCATCTCA ATGGGGGACA CAACCGGTAG
   TX_ORF2.seq  AAACTGGCAG AGGGTGATCC GGTCATCTCG ATGGGAGACA CAAATGGTAG
   MN_ORF2.seq  AAATTAACAG AAGGAGACCC GGTCGTCTCT ATGGGAGATG TGACAGGGAG
     Consensus  AAccTggCAG AgGGtGAcCC GGTCaTCTCa ATGGGgGAca caAccGGtAG

                1801                                               1850
  TAstV2_2.seq  GAGGGCTGCA CTCTTTTATA GGACTAGTGA TGAAAAATAT ATTTTATTTT
   CA_ORF2.seq  GAGGGCTGCA CTCTTTTATA GGACTAGTGA TGAGAAATAC ATTTTATTTT
   PA_ORF2.seq  GAGGGCTGCA CTCTTTTATA GGACTAGTGA TGAAAAATAT ATTTTATTTT
   MI_ORF2.seq  GAGGGCTGCA CTCTTTTATA GGACTAGTGA TGAAAAATAT ATTTTATTTT
   TX_ORF2.seq  GAGAGCTGCA CTTTTTTATA GGACTAGTGA TGAAAGGTAC ATTTTGTTCT
   MN_ORF2.seq  AAGAGCAGCA CTCTTTTATA GAACTAGTGA TGAGAGGTAC ATCTTGCTCA
     Consensus  gAGgGCtGCA CTcTTTTATA GgACTAGTGA TGAaAaaTAc ATtTTatTtt

                1851                                               1900
  TAstV2_2.seq  TCTCAACCAC AGAAGATCCA GGGGCACAGT ATCAAAATCT GAAAATGTTG
   CA_ORF2.seq  TCTCAACCAC AGAAGATCCA GGGGCACAGT ATCAAAATCT GAAAATGTTG
   PA_ORF2.seq  TCTCAACTAC AGAAGATCCA GGGGCACAGT ATCAAAATCT GAAAATGTTG
   MI_ORF2.seq  TCTCAACCAC AGAAGATCCA GGTGCACAGT ATCAAAATTT GAAAATGCTG
   TX_ORF2.seq  TTTCAACAAC AGGAGATCCA GGGTCACAAT TTGAAAATTT GAAGATGTTG
   MN_ORF2.seq  TTTCATCAAC AGAAGATCCC GGGTCACAAT TTGAGAGGCT GAAGGTGACA
     Consensus  TcTCAaC.AC AGaAGATCCa GGggCACAgT aTcAaAatcT GAAaaTGttg

                1901                                               1950
  TAstV2_2.seq  TACTTCTGGA ACTGGTCCTA TTCTGACACA AAACAGCAAT TTTTGGACCA
   CA_ORF2.seq  TACTTTTGGA ACTGGTCCTA TTCTGACACG AAACAGCAAT TTTTGGACCA
   PA_ORF2.seq  TACTTTTGGA ACTGGTCCTA TTCTGACACG AAACAGCAAT TTTTGGACCA
   MI_ORF2.seq  TACTTTTGGA ACTGGTCCTA CTCTGACACT AAACAGCAAT TTTTGGACCA
   TX_ORF2.seq  TACTTTTGGA ACTGGTCCTA TTCTGACAAC AAACAGCAAT TTCTGGACCG
   MN_ORF2.seq  ACTTTCTGGA ACTGGTCCCT TTCTGACAAC AAAAGTGAGT TCTTAAATAG
     Consensus  tacTTtTGGA ACTGGTCCta tTCTGACAc. AAAcagcAaT TttTggAcca

                1951                                               2000
  TAstV2_2.seq  CCTTAGAACA GTGCAGTTTG CAAATTTGGA TGACAGCCAG CCAGCCCCCT
   CA_ORF2.seq  CCTTAGAACA GTGCAGTTTG CAAATTTGGA TGACAGCCAT CCAGCCCCCT
   PA_ORF2.seq  CCTCAGAACA GTGCAGTTTG CAAATTTGGA TGACAACCAT CCAGCCCCCT
   MI_ORF2.seq  CCTTAGAACA GTGCAGTTCG CAAATTTGGA TGACAGCCAG CTAGCCCCCT
   TX_ORF2.seq  CCTTAGAACA GTGCAATTTG CAAATGCGGA TGACAGCCAG CCAACCCCTT
   MN_ORF2.seq  GTTGAGAACC ATACAGTATG CAAATGCACA TCAAGAAGAA ATGTCTCATT
     Consensus  ccTtAGAACa gTgCAgTttG CAAATttggA TgAcagccA. ccagCcCccT

                2001                                               2050
  TAstV2_2.seq  ATGATAGTGA TGATGATGAC CTTTCTGATG TAACATCACT TTTTGAGCAG
   CA_ORF2.seq  ATGATAGTGA TGATGATGAC CTTTCTGATG TAACATCACT TTTTGAGCAG
   PA_ORF2.seq  ATGATAGTGA TGATGATGAC CTTTCTGATG TAACATCACT TTTTGAGCAG
   MI_ORF2.seq  ATGATAGTGA TGATGATGAC CTTTCTGATG TAACATCACT TTTTGAGCAG
   TX_ORF2.seq  GTGATAGTGA TGATGATGAC CTCTCTGATG TAACATCACT CTTTGAGCAG
   MN_ORF2.seq  GTGATAGCGA CGATGATGGG CTGTCAGATG TAACGTCGCT GTTTGAACAG
     Consensus  aTGATAGtGA tGATGATGac CTtTCtGATG TAACaTCaCT tTTTGAgCAG
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               2051                                               2100
TAstV2_2.seq   GCTGATTTGG GGGATGAGAC AGACTTCAAA TTTAATATGT CCATCCAAAC
 CA_ORF2.seq   GCTGATTTGG GGGATGAGAC AGACTTCAAA TTTAATATGT CCATCCAAAC
 PA_ORF2.seq   GCTGATTTGG GGGATGAGAC AGACTTCAAA TTTAATATGT CCATCCAAAC
 MI_ORF2.seq   GCTGATTTGG GGGATGAGAC AGATTTCAAA TTTAACATGT CCATCCAAAC
 TX_ORF2.seq   GCTGATTTGG GGGATGAGAC AGATTTCAAA TTTAATATGT CCATCCAGAC
 MN_ORF2.seq   GCCGACCTGG AGGATGAGAC AGATTTTAAA TTTAAAATGT CTATTCAAAC
   Consensus   GCtGAttTGG gGGATGAGAC AGAtTTcAAA TTTAAtATGT CcATcCAaAC

               2101                                               2150
TAstV2_2.seq   CTCCAAACAT CTTGAGGAGG AGAAAAATTA CTGGAAAAAC CAGTGTGAGA
 CA_ORF2.seq   CTCCAAACAT CTTGAGGAGG AGAAAAATTA CTGGAAAAAC CAGTGTGAGA
 PA_ORF2.seq   CTCCAAACAT CTTGAGGAGG AGAAAAATTA CTGGAAAAAC CAGTGTGAGA
 MI_ORF2.seq   CTCCAAACAT CTTGAGGAGG AGAAAAATTA CTGGAAGAAC CAGTGTGAGA
 TX_ORF2.seq   CTCCAAACAT CTTGAGGAGG AGAAAAATTA CTGGAAAAAC CAGTGTGAGA
 MN_ORF2.seq   CTCTAAAGAT CTTGAGGATG AGAAAAATTA CTGGAAAAAC CAGTGTGAGA
   Consensus   CTCcAAAcAT CTTGAGGAgG AGAAAAATTA CTGGAAaAAC CAGTGTGAGA

               2151                                               2200
TAstV2_2.seq   GGATGATGAT GGAGAAGGCC CTTTCGGGCA CCTCACAGCC TCTTGTCCGG
 CA_ORF2.seq   GGATGATGAT GGAGAAGGCC CTTTCGGGCA CCTCACAGCC TCTTGTCCGG
 PA_ORF2.seq   GGATGATGAT GGAGAAGGCC CTTTCGGGCA CCTCACAGCC TCTTGTCCGG
 MI_ORF2.seq   GGATGATGAT GGAGAAGGCC CTTTCGGGCA CCTCACAGCC TCTTGTCCGG
 TX_ORF2.seq   GGATGATGAT GGAGAAGGCC CTCTCGGGCA CCTCACAACC TCTTGTCCGG
 MN_ORF2.seq   GGATGATGAT GGAGAAGGCC CTTTCGGGCA CCTCACAGCC TCTTGTCCGG
   Consensus   GGATGATGAT GGAGAAGGCC CTtTCGGGCA CCTCACAgCC TCTTGTCCGG

               2201                                               2250
TAstV2_2.seq   TTTGAGAAAG CTGGACCTAG GGCAGACCAA TCTTCTGCCA GTGGTCATTC
 CA_ORF2.seq   TTTGAGAAAG CTGGACCTAG GGCAGACCAA TCTTCTGCCA GTGGTCATTC
 PA_ORF2.seq   TTTGAGAAAG CTGGACCTAG GGCAGACCAA TCTTCTGCCA GTGGTCATTC
 MI_ORF2.seq   TTTGAGAAAG CTGGACCTAG GGCAGATCAA TCTTCTGCCA GTGGTCATTC
 TX_ORF2.seq   TTTGAGAAAG CTGGACTTAG GGCAGACCAA TCTTCTGCCA GTGGTCATTC
 MN_ORF2.seq   TTTGAGAAAG CTGGACCTAG GGCAGACCAA TCTTCTGCCA GTGGTCATTT
   Consensus   TTTGAGAAAG CTGGACcTAG GGCAGAcCAA TCTTCTGCCA GTGGTCATTc

               2251
TAstV2_2.seq   TTGA.
 CA_ORF2.seq   TTGAA
 PA_ORF2.seq   TTGAA
 MI_ORF2.seq   TTGAG
 TX_ORF2.seq   TTGA.
 MN_ORF2.seq   TTGA.
   Consensus   TTGA.
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>Canada_ORF1b.seq
GAAGTTAGAAGATCATGTGGTCAGTGGAGAGTGTCAAAAAAACTAATAGAGGGGCCTGTGACAACAAAGGCCCCTACCCC
CGTACCAGATTGGCTTAAAATATTTGCATGGGAAGATGATATATTACCACCCGAAGGAAAAATCGCATTGCCAGAAAATG
TCACTCTAATCGGGCATATACCAGTTGACAAGTTGGTTTCACGTACCAAGAAAGTCCAGGACCCATTGTTAGGCCTTGTA
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Fig 2D

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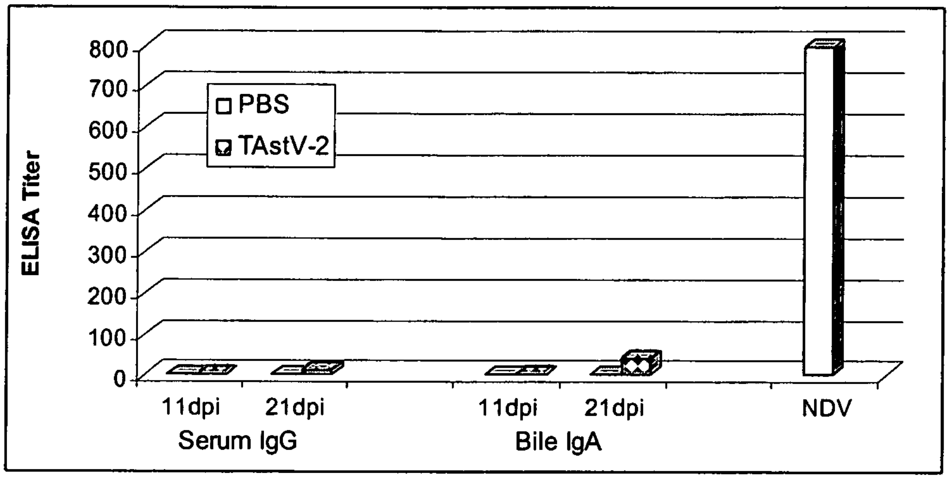
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Bile IgA
NDV

Fig3

pFastBac/TAstVcapsid

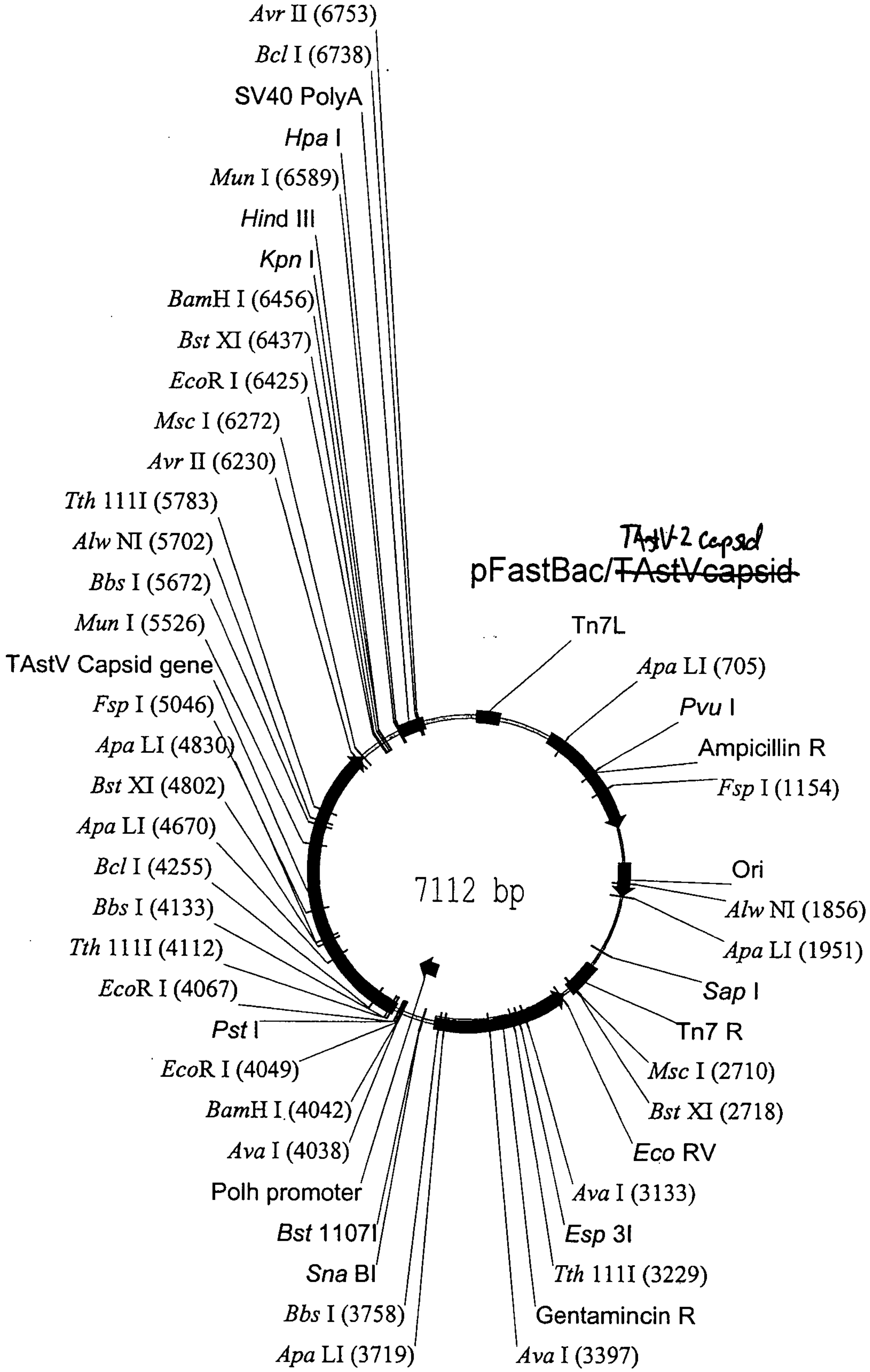
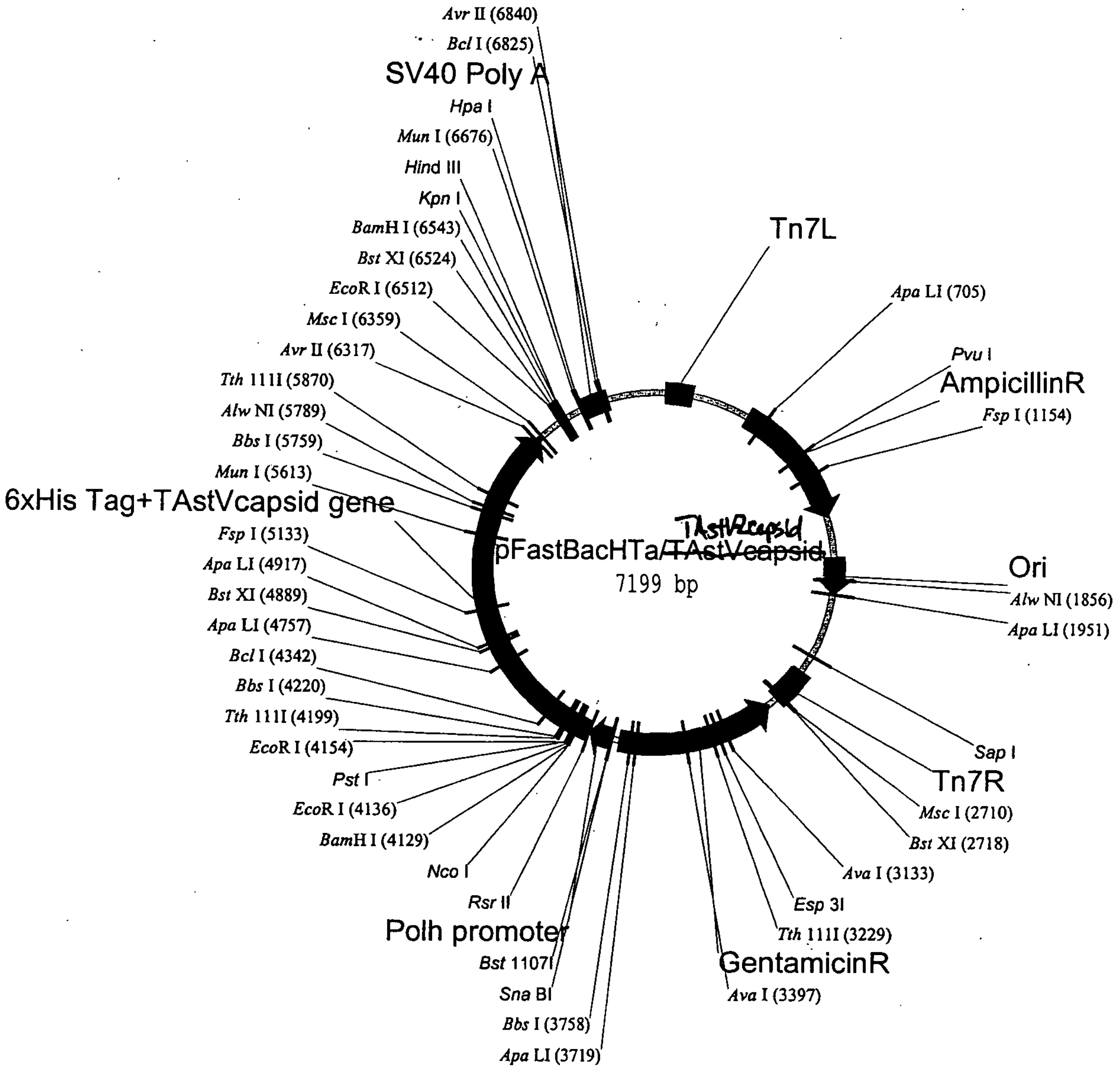


Fig 4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Bcl I (6825)
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Hpa I
Mun I (6676)
Hind III
Kpn I
BamH I (6543)
Bst XI (6524)
EcoR I (6512)
Msc I (6359)
Avr II (6317)
Tth 111I (5870)
Alw NI (5789)
Bbs I (5759)
Mun I (5613)
6xHis Tag+TAstVcapsid gene
Fsp I (5133)
Apa LI (4917)
Bst XI (4889)
Apa LI (4757)
Bcl I (4342)
Bbs I (4220)
Tth 111I (4199)
EcoR I (4154)
Pst I
EcoR I (4136)
BamH I (4129)
Nco I
Rsr II
Polh promoter
Bst 1107I
Sna BI
Bbs I (3758)
Apa LI (3719)
Tn7L
Apa LI (705)
Pvu I
AmpicillinR
Fsp I (1154)
TAstVcapsid
pFastBacHTa/~~TAstVcapsid~~
7199 bp
Ori
Alw NI (1856)
Apa LI (1951)
Sap I
Tn7R
Msc I (2710)
Bst XI (2718)
Ava I (3133)
Esp 3I
Tth 111I (3229)
GentamicinR
Ava I (3397)

pcDNA3.1-/TAstVcapsid(clone10)